Amendments to the Abstract

Please replace the abstract with the following amended abstract:

Methods of ~~identifying changes in~~ estimating genomic DNA copy number are disclosed. ~~Methods for identifying homozygous deletions and genetic amplifications are disclosed~~. Amplified genomic DNA is hybridized to an array of allele specific SNP probes to generate a hybridization pattern. A value, *S*, is calculated for individual SNPs in the experimental sample, where *S* is the log of the arithmetic average of the intensities of the perfect match probes for the SNP. *S* is calculated for the SNP in reference samples that are matched to the experimental sample in genotype. The mean and standard deviation for the S values of the reference samples are calculated and a log intensity difference is calculated by subtracting the mean values for the reference and experimental samples. The copy number of the SNP region is estimated using the difference between the mean for the SNP in the reference samples and the *S* value for the SNP in the experimental sample in a log-log linear model. ~~An array of probes designed to detect presence or absence of a plurality of different sequences is also disclosed. The probes are designed to hybridize to sequences that are predicted to be present in a reduced complexity sample. The methods may be used to detect copy number changes in cancerous tissue compared to normal tissue. The methods may be used to diagnose cancer and other diseases associated with chromosomal anomalies~~.